

SEQUENCE LISTING

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<120> Gamma-Conopeptides

<130> 2314-147-sq2

<140>

<141>

<150> US 60/069,706

<151> 1997-12-16

<160> 47

<170> PatentIn Ver. 2.0

<210> 1

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:generic formula  
of gamma-conopeptides

<220>

<221> PEPTIDE

<222> (1)..(13)

<223> Xaa at residues 1, 2, 3, 4, 5, and 6 may be  
des-Xaa or any amino acid; Xaa at residues 8, 9,  
10, 11 and 12 may be any amino acid; Xaa at  
residue 13 may be des-Xaa or any amino acid.

<220>

<221> PEPTIDE

<222> (15)..(19)

<223> Xaa at residues 15, 16, 17 and 18 may be any amino  
acid; Xaa at residue 19 is Glu,  
gamma-carboxyglutamate or Gln.

<220>

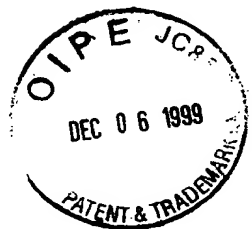
<221> PEPTIDE

<222> (22)..(28)

<223> Xaa at residues 22, 23 and 24 may be any amino  
acid; Xaa at residue 25 may be des-Xaa or any  
amino acid; Xaa at residues 27, 28 and 29 may be  
any amino acid.

<220>

<221> PEPTIDE



af

1,0320

<222> (30)..(42)

<223> Xaa at residues 30, 31 and 32 may be des-Xaa or any amino acid; Xaa at residues 34, 35, 36, 37, 38, 39, 40, 41 and 42 may be des-Xaa or any amino acid.

<400> 1

Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa  
1 5 10 15

Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa  
20 25 30

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
35 40

<210> 2

<211> 42

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:generic sequence of gamma-conopeptides.

<220>

<221> PEPTIDE

<222> (1)..(13)

<223> Xaa at residues 1, 2, 3, 4, 5 and 6 may be des-Xaa or any amino acid; Xaa at residues 8, 9, 10, 11 and 12 may be any amino acid; Xaa at residue 13 may be des-Xaa or any amino acid.

<220>

<221> PEPTIDE

<222> (15)..(22)

<223> Xaa at residues 15, 16, 17 and 18 may be any amino acid; Xaa at residue 19 is Glu, gamma-carboxyglutamate or Gln; Xaa at residue 22 is Ser or Thr.

<220>

<221> PEPTIDE

<222> (23)..(29)

<223> Xaa at residues 23 and 24 may be any amino acid; Xaa at residue 25 may be des-Xaa or any amino acid; Xaa at residues 27, 28 and 29 may be any amino acid.

<220>

<221> PEPTIDE

<222> (30)..(42)

<223> Xaa at residues 30, 31 and 32 may be des-Xaa or any amino acid; Xaa at residues 34, 35, 36, 37, 38, 39, 40, 41 and 42 may be des-Xaa or any amino acid.

<400> 2

Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa  
1 5 10 15

Xaa Xaa Xaa Cys Cys Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa  
20 25 30

Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
35 40

<210> 3  
<211> 39  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:generic formula  
of gamma-conopeptides

<220>  
<221> PEPTIDE  
<222> (1)..(13)  
<223> Xaa at residue 1 is any amino acid; Xaa at  
residues 2, 3, 4, 5 and 6 may be des-Xaa or any  
amino acid; Xaa at residues 8, 9, 10, 11, 12 and  
13 may be any amino acid.

<220>  
<221> PEPTIDE  
<222> (27)..(39)  
<223> Xaa at residues 27, 28, 29, 31, 32, 33, 34, 35, 36  
and 37 may be any amino acid; Xaa at residues 38  
and 39 may be des-Xaa or any amino acid.

<220>  
<221> PEPTIDE  
<222> (15)..(19)  
<223> Xaa at residues 15, 16, 17 and 18 may be any amino  
acid; Xaa at residue 19 is Glu or  
gamma-carboxyglutamate.

<400> 3  
Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa  
1 5 10 15

Xaa Xaa Xaa Cys Cys Ser Asn Ser Cys Asp Xaa Xaa Xaa Cys Xaa Xaa  
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
35

<210> 4  
<211> 39  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:generic  
sequence of gamma-conopeptides.

<220>  
<221> PEPTIDE  
<222> (1)..(13)  
<223> Xaa at residue 1 is any amino acid; Xaa at  
residues 2, 3, 4, 5 and 6 may be des-Xaa or any  
amino acid; Xaa at residues 8, 9, 10, 11, 12 and  
13 may be any amino acid.

<220>

<221> PEPTIDE  
<222> (15)..(19)  
<223> Xaa at residue 15 is Ser or Thr; Xaa at residues  
16, 17 and 18 may be any amino acid; Xaa at  
residue 19 is Glu or gamma-carboxyglutamate.

<220>  
<221> PEPTIDE  
<222> (27)..(39)  
<223> Xaa at residues 27, 28, 29, 31, 32, 33, 34, 35, 36  
and 37 may be any amino acid; Xaa at residues 38  
and 39 may be des-Xaa or any amino acid.

<400> 4  
Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa  
1 5 10 15

Xaa Xaa Xaa Cys Cys Ser Asn Ser Cys Asp Xaa Xaa Xaa Cys Xaa Xaa  
20 25 30

Xaa Xaa Xaa Xaa Xaa Xaa Xaa  
35

<210> 5  
<211> 34  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:generic  
sequence of gamma-conopeptides.

<220>  
<221> PEPTIDE  
<222> (1)..(6)  
<223> Xaa at residues 1 and 2 may be des-Xaa or any  
amino acid; Xaa at residue 3 is Asp, Glu or  
gamma-carboxyglutamate; Xaa at residues 5 and 6  
may be any amino acid.

<220>  
<221> PEPTIDE  
<222> (7)..(16)  
<223> Xaa at residue 7 is Trp or 6-bromo-Trp; Xaa at  
residues 9, 10, 13 and 14 may be any amino acid;  
Xaa at residue 16 is Glu or  
gamma-carboxyglutamate.

<220>  
<221> PEPTIDE  
<222> (28)..(34)  
<223> Xaa at residues 28, 30, 31, 32, 33 and 34 may be  
any amino acid.

<400> 5  
Xaa Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Cys Thr Xaa Xaa Ser Xaa  
1 5 10 15

Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Xaa Xaa Xaa  
20 25 30

Xaa Xaa

<210> 6  
 <211> 32  
 <212> PRT  
 <213> Conus pennaceus

<220>  
 <221> PEPTIDE  
 <222> (1)..(31)  
 <223> Xaa at residue 5 is Trp or 6-bromo-Trp; Xaa at residues 14 and 26 are Glu or gamma-carboxyglutamate; Xaa at residue 31 is Pro or hydroxy-Pro.

<400> 6  
 Asp Cys Thr Ser Xaa Phe Gly Arg Cys Thr Val Asn Ser Xaa Cys Cys  
 1 5 10 15  
 Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Tyr Ala Phe Xaa Ser  
 20 25 30

<210> 7  
 <211> 34  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(34)  
 <223> Xaa at residues 1, 7 and 34 are Trp or 6-bromo-Trp; Xaa at residues 3 and 16 are Glu or gamma-carboxyglutamate; Xaa at residues 31 and 32 are Pro or hydroxy-Pro.

<400> 7  
 Xaa Leu Xaa Cys Ser Val Xaa Phe Ser His Cys Thr Lys Asp Ser Xaa  
 1 5 10 15  
 Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Xaa Xaa  
 20 25 30

Asp Xaa

<210> 8  
 <211> 39  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(39)  
 <223> Xaa at residues 1, 2, 4, 10 and 39 are Trp or 6-bromo-Trp ; Xaa at residues 19 and 31 are Glu or gamma-carboxyglutamate; Xaa at residues 34, 36 and 37 are Pro or hydroxy-Pro.

<400> 8  
 Xaa Xaa Arg Xaa Gly Gly Cys Met Ala Xaa Phe Gly Leu Cys Ser Arg

1                      5                      10                      15  
 Asp Ser Xaa Cys Cys Ser Asn Ser Cys Asp Val Thr Arg Cys Xaa Leu  
                     20                      25                      30

Met Xaa Phe Xaa Xaa Asp Xaa  
                     35

<210> 9  
 <211> 27  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residues 9, 13 and 17 are Glu or  
                     gamma-carboxyglutamate.

<400> 9  
 Cys Lys Thr Tyr Ser Lys Tyr Cys Xaa Ala Asp Ser Xaa Cys Cys Thr  
                     1                      5                      10                      15

Xaa Gln Cys Val Arg Ser Tyr Cys Thr Leu Phe  
                     20                      25

<210> 10  
 <211> 34  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(34)  
 <223> Xaa at residues 2, 3, 10 and 32 are Trp or  
                     6-bromo-Trp; Xaa at residues 18, 26 and 33 are Glu  
                     or gamma-carboxyglutamate; Xaa at residue 12 is  
                     Pro or hydroxy-Pro.

<400> 10  
 Asp Xaa Xaa Asp Asp Gly Cys Ser Val Xaa Gly Xaa Cys Thr Tyr Asn  
                     1                      5                      10                      15

Ala Xaa Cys Cys Ser Gly Asp Cys His Xaa Thr Cys Ile Phe Gly Xaa  
                     20                      25                      30

Xaa Val

<210> 11  
 <211> 31  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(31)  
 <223> Xaa at residues 3 and 31 are Trp of 6-bromo-Trp;  
                     Xaa at residues 5, 18, 22 and 25 are Glu or  
                     gamma-carboxyglutamate; Xaa at residue 16 is Pro  
                     or hydroxy-Pro.

<400> 11  
Gly Met Xaa Gly Xaa Cys Lys Asp Gly Leu Thr Thr Cys Leu Ala Xaa  
1 5 10 15

Ser Xaa Cys Cys Ser Xaa Asp Cys Xaa Gly Ser Cys Thr Met Xaa  
20 25 30

<210> 12  
<211> 32  
<212> PRT  
<213> Conus gloriamaris

<220>  
<221> PEPTIDE  
<222> (1)..(32)  
<223> Xaa at residue 5 is Trp or 6-bromo-Trp; Xaa at  
residue 1 is Glu or gamma-carboxyglutamate; Xaa at  
residues 8 and 11 are Pro or hydroxy-Pro.

<400> 12  
Xaa Cys Arg Ala Xaa Tyr Ala Xaa Cys Ser Xaa Gly Ala Gln Cys Cys  
1 5 10 15

Ser Leu Leu Met Cys Ser Lys Ala Thr Ser Arg Cys Ile Leu Ala Leu  
20 25 30

<210> 13  
<211> 29  
<212> PRT  
<213> Conus marmoreus

<220>  
<221> PEPTIDE  
<222> (1)..(29)  
<223> Xaa at residues 8 and 15 are Trp or 6-bromo-Trp;  
Xaa at residues 5, 16 and 23 are Glu or  
gamma-carboxyglutamate; Xaa at residue 10 is Pro  
or hydroxy-Pro.

<400> 13  
Asn Gly Gln Cys Xaa Asp Val Xaa Met Xaa Cys Thr Ser Asn Xaa Xaa  
1 5 10 15

Cys Cys Ser Leu Asp Cys Xaa Met Tyr Cys Thr Gln Ile  
20 25

<210> 14  
<211> 27  
<212> PRT  
<213> Conus marmoreus

<220>  
<221> PEPTIDE  
<222> (1)..(27)  
<223> Xaa at residue 4 is Trp or 6-bromo-Trp; Xaa at  
residues 9, 12, 13 and 17 are Glu or  
gamma-carboxyglutamate.

<400> 14  
Cys Gly Gly Xaa Ser Thr Tyr Cys Xaa Val Asp Xaa Xaa Cys Cys Ser  
1 5 10 15

Xaa Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe  
20 25

<210> 15  
<211> 26  
<212> PRT  
<213> Conus marmoreus

<220>  
<221> PEPTIDE  
<222> (1)..(26)  
<223> Xaa at residues 8 and 15 are Trp or 6-bromo-Trp;  
Xaa at residue 16 is Glu or  
gamma-carboxyglutamate.

<400> 15  
Asn Gly Gly Cys Lys Ala Thr Xaa Met Ser Cys Ser Ser Gly Xaa Xaa  
1 5 10 15

Cys Cys Ser Met Ser Cys Asp Met Tyr Cys  
20 25

<210> 16  
<211> 323  
<212> DNA  
<213> Conus textile

<220>  
<221> CDS  
<222> (1)..(153)

<400> 16  
gaa cgg gct aag atc aac ttg ctt cca aag aga aag cca cct gct gag 48  
Glu Arg Ala Lys Ile Asn Leu Leu Pro Lys Arg Lys Pro Pro Ala Glu  
1 5 10 15

cgt tgg ttg gaa tgc agt gtt tgg ttt tca cat tgt acg aag gac tgc 96  
Arg Trp Leu Glu Cys Ser Val Trp Phe Ser His Cys Thr Lys Asp Ser  
20 25 30

gaa tgt tgt tct aat agt tgt gac caa acg tac tgc acg tta atg cca 144  
Glu Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Pro  
35 40 45

ccg gac tgg tgacatcgcc actctcctgt tcagagtctt caaggctttt 193  
Pro Asp Trp  
50

gttctctttt gaagaatttt aacgagtga caaaaaagtg gactagcatg tttccttttc 253  
cctttgcaaa atcaatgatg gaggtaaaag cctcccattt tgtcttcatc aataaagaac 313  
ttatcatcat 323

<210> 17  
<211> 51  
<212> PRT



<213> Conus textile

<400> 17

Glu Arg Ala Lys Ile Asn Leu Leu Pro Lys Arg Lys Pro Pro Ala Glu  
1 5 10 15

Arg Trp Leu Glu Cys Ser Val Trp Phe Ser His Cys Thr Lys Asp Ser  
20 25 30

Glu Cys Cys Ser Asn Ser Cys Asp Gln Thr Tyr Cys Thr Leu Met Pro  
35 40 45

Pro Asp Trp  
50

<210> 18

<211> 510

<212> DNA

<213> Conus textile

<220>

<221> CDS

<222> (95)..(337)

<400> 18

tgactcgcca tctctctctt cagtctccct gacagctgcc ttcagtcgac cctgccgtca 60

tctcaacgca cacttgaagt gaaaaacctt tctc atg gag aaa ctg aca att ctg 115  
Met Glu Lys Leu Thr Ile Leu  
1 5

ctt ctt gtt gct gct gta ctg ttg tct atc cag gcc cta aat caa gaa 163  
Leu Leu Val Ala Ala Val Leu Leu Ser Ile Gln Ala Leu Asn Gln Glu  
10 15 20

aaa cac caa cgg gca aag atc aac ttg ctt tca aag aga aag cca cct 211  
Lys His Gln Arg Ala Lys Ile Asn Leu Leu Ser Lys Arg Lys Pro Pro  
25 30 35

gct gag cgt tgg tgg cgg tgg gga gga tgc atg gct tgg ttt ggg ctt 259  
Ala Glu Arg Trp Trp Arg Trp Gly Gly Cys Met Ala Trp Phe Gly Leu  
40 45 50 55

tgt tct agg gac tct gaa tgt tgt tct aat agt tgt gac gta acg cgc 307  
Cys Ser Arg Asp Ser Glu Cys Cys Ser Asn Ser Cys Asp Val Thr Arg  
60 65 70

tgc gag tta atg cca ttc cca cca gac tgg tgacatcgac actctcctct 357  
Cys Glu Leu Met Pro Phe Pro Pro Asp Trp  
75 80

tcagagtctt caaggctttt gttctctttt gaagaatttt tacgagttaa caaaaacgtg 417

gactagcagc tttctttttt cctttgcaaa atcaatgatg gaggtaaaag tgtcccat 477

tgtcttcctc aataaagaac ttatcatcat aat 510

<210> 19

<211> 81

<212> PRT

<213> Conus textile

40

A

<400> 19  
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Leu Ser  
1 5 10 15  
Ile Gln Ala Leu Asn Gln Glu Lys His Gln Arg Ala Lys Ile Asn Leu  
20 25 30  
Leu Ser Lys Arg Lys Pro Pro Ala Glu Arg Trp Trp Arg Trp Gly Gly  
35 40 45  
Cys Met Ala Trp Phe Gly Leu Cys Ser Arg Asp Ser Glu Cys Cys Ser  
50 55 60  
Asn Ser Cys Asp Val Thr Arg Cys Glu Leu Met Pro Phe Pro Pro Asp  
65 70 75 80  
Trp

<210> 20  
<211> 441  
<212> DNA  
<213> Conus textile

<220>  
<221> CDS  
<222> (16)..(243)

<400> 20  
ggaaaaactt ttatc atg gag aaa ctg aca atc ctg ctc ctt gtt gct gct 51  
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala  
1 5 10  
gta ctg atg tgc acc cag gcc atg ttt caa ggt gat gga gaa aaa tcc 99  
Val Leu Met Ser Thr Gln Ala Met Phe Gln Gly Asp Gly Glu Lys Ser  
15 20 25  
cgg aag gcg gag atc aac ttt tct gaa aca aga aag ttg gcg aga aac 147  
Arg Lys Ala Glu Ile Asn Phe Ser Glu Thr Arg Lys Leu Ala Arg Asn  
30 35 40  
aag cag aaa cgc tgc aaa act tat tca aag tat tgt gaa gct gac tgc 195  
Lys Gln Lys Arg Cys Lys Thr Tyr Ser Lys Tyr Cys Glu Ala Asp Ser  
45 50 55 60  
gaa tgc tgt acc gaa cag tgt gta agg tct tac tgc acg ttg ttt gga 243  
Glu Cys Cys Thr Glu Gln Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly  
65 70 75  
tgaattcgga ccacaagcca tccgatatca cccctctcct cttcagaggc ttcaaggctt 303  
ttgttatcct tttgaagaat ctttatcgag taaacataag tagacaagct ttttttttcc 363  
tttgcaaaat gaagaatgat ggcaaaaagc ccccatTTTT gtcttcatca ataaagaact 423  
cgctatcaga ataaaaaa 441

<210> 21  
<211> 76  
<212> PRT  
<213> Conus textile

[illegible]

42 A

Met	Glu	Lys	Leu	Thr	Ile	Leu	Leu	Leu	Val	Ala	Ala	Val	Leu	Met	Ser
1				5					10					15	
Thr	Gln	Ala	Leu	Ile	Gln	Asp	Gln	Arg	Gln	Lys	Ala	Lys	Ile	Asn	Leu
			20					25					30		
Phe	Ser	Lys	Arg	Gln	Ala	Tyr	Ala	Arg	Asp	Trp	Trp	Asp	Asp	Gly	Cys
		35					40					45			
Ser	Val	Trp	Gly	Pro	Cys	Thr	Val	Asn	Ala	Glu	Cys	Cys	Ser	Gly	Asp
	50					55					60				
Cys	His	Glu	Thr	Cys	Ile	Phe	Gly	Trp	Glu	Val					
65					70					75					

<210> 24  
 <211> 533  
 <212> DNA  
 <213> Conus textile

<220>  
 <221> CDS  
 <222> (110)..(337)

<400> 24  
 ctctgccggt tgacacntca tctactctct cagtctccct gacagctgcc ttcagtcgac 60  
 cctgccgtca tctcagcgca gacttgataa gaagtgaaaa acctttatc atg gag aaa 118  
 Met Glu Lys  
 1  
 ctg aca atc ctg ctt ctt gtt gct gct gta ctg atg tcg acc cag gcc 166  
 Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala  
 5 10 15  
 ctg gtt gaa cgt gct gga gaa aac cac tca aag gag aac atc aat ttt 214  
 Leu Val Glu Arg Ala Gly Glu Asn His Ser Lys Glu Asn Ile Asn Phe  
 20 25 30 35  
 tta tta aaa aga aag aga gct gct gac agg ggg atg tgg ggc gaa tgc 262  
 Leu Leu Lys Arg Lys Arg Ala Ala Asp Arg Gly Met Trp Gly Glu Cys  
 40 45 50  
 aaa gat ggg tta acg aca tgt ttg gcg ccc tca gag tgt tgt tct gag 310  
 Lys Asp Gly Leu Thr Thr Cys Leu Ala Pro Ser Glu Cys Cys Ser Glu  
 55 60 65  
 gat tgt gaa ggg agc tgc acg atg tgg tgatgaattc tgaccacaag 357  
 Asp Cys Glu Gly Ser Cys Thr Met Trp  
 70 75  
 ccattctgaca tcaccactct cctcttcaga ggcttcaagg cttttgtttt ctttttgaat 417  
 aatcttttacg agtaaacaaa taagtagact agcgcgtttt tttccctttg agaaatcaat 477  
 gatggaggta aatagcttcc tattttgtct tattcaataa agaacttatc ataata 533

<210> 25  
 <211> 76  
 <212> PRT  
 <213> Conus textile

<400> 25  
 Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser  
     1                    5                    10                    15  
 Thr Gln Ala Leu Val Glu Arg Ala Gly Glu Asn His Ser Lys Glu Asn  
                     20                    25                    30  
 Ile Asn Phe Leu Leu Lys Arg Lys Arg Ala Ala Asp Arg Gly Met Trp  
                     35                    40                    45  
 Gly Glu Cys Lys Asp Gly Leu Thr Thr Cys Leu Ala Pro Ser Glu Cys  
                     50                    55                    60  
 Cys Ser Glu Asp Cys Glu Gly Ser Cys Thr Met Trp  
                     65                    70                    75

<210> 26  
 <211> 408  
 <212> DNA  
 <213> Conus gloriamaris

<220>  
 <221> CDS  
 <222> (2)..(211)

<400> 26  
 g ctg aca atc ctg ctt ctt gtt gct gct gta ctg atg tcg acc cag gcc 49  
   Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala  
     1                    5                    10                    15  
 ctg att caa ggt ggt ggt gac aaa cgt caa aag gca aac atc aac ttt 97  
 Leu Ile Gln Gly Gly Gly Asp Lys Arg Gln Lys Ala Asn Ile Asn Phe  
                     20                    25                    30  
 ctt tca agg tgg gac cgt gag tgc agg gct tgg tat gcg ccg tgt agc 145  
 Leu Ser Arg Trp Asp Arg Glu Cys Arg Ala Trp Tyr Ala Pro Cys Ser  
                     35                    40                    45  
 cct ggc gcg caa tgt tgt agt ttg ctg atg tgt tca aaa gcg acc agc 193  
 Pro Gly Ala Gln Cys Cys Ser Leu Leu Met Cys Ser Lys Ala Thr Ser  
                     50                    55                    60

cgc tgc ata ttg gcg tta tgaactctga ccacaagcca tccgacatca 241  
 Arg Cys Ile Leu Ala Leu  
     65                    70

ccactctcct cttcagaggc ttcaaggctt tttgtttttc ttttgaagaa tctttacgag 301  
 tgaacaaata agtagaatag cacgtttttc cccctttgca aaatcaataa tggagggttaa 361  
 aaaaaaactt ctgtcttctt caataaagaa gttatcataa taaaaaa 408

<210> 27  
 <211> 70  
 <212> PRT  
 <213> Conus gloriamaris

<400> 27  
 Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala  
   1                    5                    10                    15  
 Leu Ile Gln Gly Gly Gly Asp Lys Arg Gln Lys Ala Asn Ile Asn Phe

	20		25		30
Leu Ser Arg Trp Asp Arg Glu Cys Arg Ala Trp Tyr Ala Pro Cys Ser	35	40	45		
Pro Gly Ala Gln Cys Cys Ser Leu Leu Met Cys Ser Lys Ala Thr Ser	50	55	60		
Arg Cys Ile Leu Ala Leu	65	70			

<210> 28  
 <211> 278  
 <212> DNA  
 <213> Conus marmoreus

<220>  
 <221> CDS  
 <222> (4)..(222)

<400> 28	
atc atg cag aaa ctg ata atc ctg ctt ctt gtt gct gct gtg ctg ctg	48
Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Leu	
1 5 10 15	
tcg acc cag gcc cta aat caa gaa aaa cgc cca aag gag atg atc aat	96
Ser Thr Gln Ala Leu Asn Gln Glu Lys Arg Pro Lys Glu Met Ile Asn	
20 25 30	
ttt tta tca aaa gga aag aca aat gct gag agg cgg aac ggc caa tgc	144
Phe Leu Ser Lys Gly Lys Thr Asn Ala Glu Arg Arg Asn Gly Gln Cys	
35 40 45	
gag gat gtt tgg atg cct tgt aca tcg aac tgg gaa tgc tgt tct ttg	192
Glu Asp Val Trp Met Pro Cys Thr Ser Asn Trp Glu Cys Cys Ser Leu	
50 55 60	
gat tgt gaa atg tac tgc aca cag ata gga tgaactctga ccacaagcca	242
Asp Cys Glu Met Tyr Cys Thr Gln Ile Gly	
65 70	

tccgacatca ccactctcct cttcagagtc ttcaag	278
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<210> 29  
 <211> 73  
 <212> PRT  
 <213> Conus marmoreus

<400> 29	
Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Leu Ser	
1 5 10 15	
Thr Gln Ala Leu Asn Gln Glu Lys Arg Pro Lys Glu Met Ile Asn Phe	
20 25 30	
Leu Ser Lys Gly Lys Thr Asn Ala Glu Arg Arg Asn Gly Gln Cys Glu	
35 40 45	
Asp Val Trp Met Pro Cys Thr Ser Asn Trp Glu Cys Cys Ser Leu Asp	
50 55 60	
Cys Glu Met Tyr Cys Thr Gln Ile Gly	

65

70

<210> 30  
<211> 287  
<212> DNA  
<213> Conus marmoreus

<220>  
<221> CDS  
<222> (4)..(231)

<400> 30  
atc atg gag aaa ctg aca atc ctg ctt ctt gtt gct gct gta ctg ata 48  
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Ile  
1 5 10 15  
ccg acc cag gcc ctt ttt caa ggt gat gac gga aaa tcc cag aag gcg 96  
Pro Thr Gln Ala Leu Phe Gln Gly Asp Asp Gly Lys Ser Gln Lys Ala  
20 25 30  
gag atc aag tct ttt gaa aca aga aag tta gcg aga aac aag cag gta 144  
Glu Ile Lys Ser Phe Glu Thr Arg Lys Leu Ala Arg Asn Lys Gln Val  
35 40 45  
cgc tgc ggt ggt tgg tca acg tat tgt gaa gtt gac gag gaa tgc tgt 192  
Arg Cys Gly Gly Trp Ser Thr Tyr Cys Glu Val Asp Glu Glu Cys Cys  
50 55 60  
tcg gaa tca tgt gta agg tct tac tgc acg ctg ttt gga tgaactcgga 241  
Ser Glu Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly  
65 70 75  
ccacaagcca tccgatatca ccactctcct gttcagagtc ttcaag 287

<210> 31  
<211> 76  
<212> PRT  
<213> Conus marmoreus

<400> 31  
Met Glu Lys Leu Thr Ile Leu Leu Leu Val Ala Ala Val Leu Ile Pro  
1 5 10 15  
Thr Gln Ala Leu Phe Gln Gly Asp Asp Gly Lys Ser Gln Lys Ala Glu  
20 25 30  
Ile Lys Ser Phe Glu Thr Arg Lys Leu Ala Arg Asn Lys Gln Val Arg  
35 40 45  
Cys Gly Gly Trp Ser Thr Tyr Cys Glu Val Asp Glu Glu Cys Cys Ser  
50 55 60  
Glu Ser Cys Val Arg Ser Tyr Cys Thr Leu Phe Gly  
65 70 75

<210> 32  
<211> 278  
<212> DNA  
<213> Conus marmoreus

<220>

<221> CDS  
<222> (4)..(213)

<400> 32  
atc atg cag aaa ctg ata att ctg ctt ctt gtt gct gct gtg ctg atg 48  
Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met  
1 5 10 15  
acg acc cag gcc cta tat caa gaa aaa cgc cga aag gag atg atc aat 96  
Thr Thr Gln Ala Leu Tyr Gln Glu Lys Arg Arg Lys Glu Met Ile Asn  
20 25 30  
ttt tta tca aaa gga aag ata aat gct gag agg cgg aac ggc gga tgc 144  
Phe Leu Ser Lys Gly Lys Ile Asn Ala Glu Arg Arg Asn Gly Gly Cys  
35 40 45  
aaa gct act tgg atg tct tgt tca tgc ggc tgg gaa tgc tgt tct atg 192  
Lys Ala Thr Trp Met Ser Cys Ser Ser Gly Trp Glu Cys Cys Ser Met  
50 55 60  
agt tgt gac atg tac tgc gga tagataggat gaactctgac cacaagccat 243  
Ser Cys Asp Met Tyr Cys Gly  
65 70  
ccgacatcac cactctcctc ttcagagtct tcaag 278

<210> 33  
<211> 70  
<212> PRT  
<213> Conus marmoreus

<400> 33  
Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Thr  
1 5 10 15  
Thr Gln Ala Leu Tyr Gln Glu Lys Arg Arg Lys Glu Met Ile Asn Phe  
20 25 30  
Leu Ser Lys Gly Lys Ile Asn Ala Glu Arg Arg Asn Gly Gly Cys Lys  
35 40 45  
Ala Thr Trp Met Ser Cys Ser Ser Gly Trp Glu Cys Cys Ser Met Ser  
50 55 60  
Cys Asp Met Tyr Cys Gly  
65 70

<210> 34  
<211> 528  
<212> DNA  
<213> Conus textile

<220>  
<221> CDS  
<222> (98)..(316)

<400> 34  
gcacgtcatc ttctctctca gtctgcctga cagctgcctt cagtcacccc tgccgtcatc 60  
tcagcgtaga cttggtaaga agtgaaaaac atttatac atg cag aaa ctg ata atc 115  
Met Gln Lys Leu Ile Ile  
1 5



ctg ctt ctt gtt gct gct gtg ctg atg tgc acc cag gcc gtg ctt caa 163  
 Leu Leu Leu Val Ala Ala Val Leu Met Ser Thr Gln Ala Val Leu Gln  
                   10                  15                  20

gaa aaa cgc cca aag gag aag atc aag ctt tta tca aag aga aag aca 211  
 Glu Lys Arg Pro Lys Glu Lys Ile Lys Leu Leu Ser Lys Arg Lys Thr  
                   25                  30                  35

gat gct gag aag cag cag aag cgc ctt tgc ccg gat tac acg gag cct 259  
 Asp Ala Glu Lys Gln Gln Lys Arg Leu Cys Pro Asp Tyr Thr Glu Pro  
                   40                  45                  50

tgt tca cat gcc cat gaa tgc tgt tca tgg aat tgt tat aat ggg cac 307  
 Cys Ser His Ala His Glu Cys Cys Ser Trp Asn Cys Tyr Asn Gly His  
                   55                  60                  65                  70

tgt acg gga tgaactcgga ccacaagcca tccgacatca ccactctcct 356  
 Cys Thr Gly

cttcagagggc ttcaagactt ttgtttctgat tttggacaat ctttacgagt aaacaaataa 416

ttagactagc acttttttttc ccctttgcaa aatcaatgat ggaggtaaaa agcctcccat 476

tttgtcttca tcaataaaga acttatcatc aaaaaaaaaa aaaaaaaaaa aa 528

<210> 35  
 <211> 73  
 <212> PRT  
 <213> Conus textile

<400> 35  
 Met Gln Lys Leu Ile Ile Leu Leu Leu Val Ala Ala Val Leu Met Ser  
           1                  5                  10                  15

Thr Gln Ala Val Leu Gln Glu Lys Arg Pro Lys Glu Lys Ile Lys Leu  
                   20                  25                  30

Leu Ser Lys Arg Lys Thr Asp Ala Glu Lys Gln Gln Lys Arg Leu Cys  
                   35                  40                  45

Pro Asp Tyr Thr Glu Pro Cys Ser His Ala His Glu Cys Cys Ser Trp  
           50                  55                  60

Asn Cys Tyr Asn Gly His Cys Thr Gly  
           65                  70

<210> 36  
 <211> 26  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(26)  
 <223> Xaa at residue 18 is Trp or 6-bromo-Trp; Xaa at  
           residues 7 and 14 are Glu or  
           gamma-carboxyglutamate; Xaa at residues 3 and 8  
           are Pro or hydroxy-Pro.

<400> 36  
 Leu Cys Xaa Asp Tyr Thr Xaa Xaa Cys Ser His Ala His Xaa Cys Cys  
           1                  5                  10                  15

Ser Xaa Asn Cys Tyr Asn Gly His Cys Thr  
20 25

<210> 37  
<211> 4  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
gamma-conopeptide sequence for probe

<220>  
<221> PEPTIDE  
<222> (1)  
<223> Xaa is Glu or Gln.

<400> 37  
Xaa Cys Cys Ser  
1

<210> 38  
<211> 12  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:degenerate  
probe for consensus gamma-conopeptide sequence.

<400> 38  
sartgytggya gy

12

<210> 39  
<211> 12  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:degenerate  
probe for consensus gamma-conopeptide sequence.

<400> 39  
sartgytgyt cn

12

<210> 40  
<211> 8  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:consensus  
pro-gamma-conopeptide sequence for probe.

<400> 40  
Ile Leu Leu Val Ala Ala Val Leu  
1 5

<210> 41

<211> 24  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:degenerate  
 probe for consensus pro-gamma-conopeptide  
 sequence.

<400> 41  
 athytntyng tngcngcngt nytn

24

<210> 42  
 <211> 32  
 <212> PRT  
 <213> Conus pennaceus

<220>  
 <221> PEPTIDE  
 <222> (1)..(31)  
 <223> Xaa at residues 14 and 26 are  
 gamma-carboxyglutamate; Xaa at residue 31 is  
 hdroxy-Pro.

<400> 42  
 Asp Cys Thr Ser Trp Phe Gly Arg Cys Thr Val Asn Ser Xaa Cys Cys  
 1 5 10 15  
 Ser Asn Ser Cys Asp Gln Thr Tyr Cys Xaa Leu Tyr Ala Phe Xaa Ser  
 20 25 30

<210> 43  
 <211> 27  
 <212> PRT  
 <213> Conus textile

<220>  
 <221> PEPTIDE  
 <222> (1)..(27)  
 <223> Xaa at residues 9 and 13 are  
 gamma-carboxyglutamate.

<400> 43  
 Cys Gly Gly Tyr Ser Thr Tyr Cys Xaa Val Asp Ser Xaa Cys Cys Ser  
 1 5 10 15  
 Asp Asn Cys Val Arg Ser Tyr Cys Thr Leu Phe  
 20 25

<210> 44  
 <211> 8  
 <212> PRT  
 <213> Conus pennaceus

<220>  
 <221> MOD\_RES  
 <222> (2)  
 <223> Xaa at residue 2 is carboxymethylCys

<400> 44  
Asp Xaa Thr Ser Trp Phe Gly Arg  
1 5

<210> 45  
<211> 24  
<212> PRT  
<213> Conus pennaceus

<220>  
<221> PEPTIDE  
<222> (1)..(24)  
<223> Xaa at residues 6 and 18 are  
gamma-carboxyglutamate; Xaa at residue 23 is  
hydroxy-Pro.

<400> 45  
Xaa Thr Val Asn Ser Xaa Xaa Xaa Ser Asn Ser Xaa Asp Gln Thr Tyr  
1 5 10 15

Xaa Xaa Leu Tyr Ala Phe Xaa Ser  
20

<210> 46  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer for M13  
universal priming site.

<400> 46  
tttcccagtc acgacggt

18

<210> 47  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:primer for M13  
reverse priming site.

<400> 47  
cacacaggaa acagctatg

19